

SEQUENCE LISTING

5 <110> Degussa-Hüls AG
 Forschungszentrum Jülich GmbH
 <120> L-Lysine-producing corynebacteria and
 process for the preparation of lysine.
 10 <130> 980183 BT
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 15 <160> 6
 <170> PatentIn Ver. 2.1
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 <211> 795
 20 <212> DNA
 <213> Corynebacterium glutamicum
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 25 <222> (774)..(779)
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 tccgggtatcg atacctggaa cgacaacctg atcaggatat ccagtgcctt gaattattgac 180
 35 gttgaggaag gaatcaccag ccatctcaac tgggaagacct gacgcctgct gaattggatc 240
 agtggcccaa tcgacccacc aaccagggtg gccattaccg gcgatatcaa aaacaactcg 300
 tgtgaacggt tcgtgctcgg caacgcggat gccagcgatc gacatatcgg agtcaccaac 360
 ttgagcctgc tgcttctgat ccatcgacgg ggaacccaac ggcggcaaag cagtggggga 420
 aggggggagt ttggtgcact ctgaaccgag tgggtctctga agtggtaggc gacggggcag 480
 ctatctgaag gcgtgcgagt tgtggtgacc gggtagcggt tttcagtttc tgtcacaact 540
 40 ggagcaggac tagcagaggt tgtaggcggt gagccgcttc catcacaagc acttaaaagt 600
 aaagaggcgg aaaccacaag cgccaaggaa ctactgcgga acgggcggtg aaggggcaact 660
 taagtctcat atttcaaaca tagttccacc tgtgtgatta atccctagaa cggaacaaac 720
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 45 ttctgaacgg gtacg 795
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 50 <213> Corynebacterium glutamicum
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 <222> (851)..(1594)

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 5 acggggttca aaaatactgg tgaagttgat gtcttcaaca atgcctgcac caggatatga 120
 tccggtatcg atacctggaa cgacaacctg atcaggatat ccagtgcctt gaatttgac 180
 10 gttgaggaag gaatcaccag ccatctcaac tggaagacct gacgcctgct gaattggatc 240
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 15 ttgagcctgc tgcttctgat ccatcgacgg ggaaccaac ggccggcaaag cagtggggga 420
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 30 ttctgaacgg gtacgtctag actggtgggc gtttgaaaaa ctcttcgccc caggaaaatg 840
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 Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg
 1 5 10
 35 gtt ggt caa act att gtg gca gca gtc aat gag tcc gac gat ctg gag 937
 Val Gly Gln Thr Ile Val Ala Val Asn Glu Ser Asp Asp Leu Glu
 15 20 25
 40 ctt gtt gca gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac 985
 Leu Val Ala Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp
 30 35 40 45
 45 aac ggc gct gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg 1033
 Asn Gly Ala Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met
 50 55 60
 50 ggc aac ctg gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga 1081
 Gly Asn Leu Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly
 65 70 75
 55 acc acg ggc ttc gat gat gct cgt ttg gag cag gtt cgc gac tgg ctt 1129
 Thr Thr Gly Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu
 80 85 90
 60 gaa gga aaa gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc 1177
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 95 100 105
 60 tct gcg gtg ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc 1225
 Ser Ala Val Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe
 110 115 120 125

gaa tca gct gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca 1273
 Glu Ser Ala Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala 140
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5 cct tca ggc acc gcg atc cac act gct cag ggc att gct gcg gca cgc 1321
 Pro Ser Gly Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Arg 155
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10 aaa gaa gca ggc atg gac gca cag cca gat gcg acc gag cag gca ctt 1369
 Lys Glu Ala Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu 170
 160 165

15 gag ggt tcc cgt ggc gca agc gta gat gga atc ccg gtt cat gca gtc 1417
 Glu Gly Ser Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val 185
 175 180

20 cgc atg tcc ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag 1465
 Arg Met Ser Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln 205
 190 195 200

ggt cag acc ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt 1513
 Gly Gln Thr Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe 220
 210 215

25 gca cca ggt gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc 1561
 Ala Pro Gly Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly 235
 225 230

30 cta gtc gta gga ctt gag cat tac cta ggc ctg taaaggctca tttcagcagc 1614
 Leu Val Val Gly Leu Glu His Tyr Leu Gly Leu 245
 240

35 ggggtggaatt ttttaaaagg agcgtttaaa ggctgtggcc gaacaagtta aattgagcgt 1674
 ggagttgata gcgtgcagtt cttttactcc acccgctgat gttgagtggc caactgatgt 1734
 tgagggcgcg gaagcactcg tcgagtttgc gggctcgtgcc tgctacgaaa cttttgataa 1794

40 gccgaaccct cgaactgctt c 1815

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 45 <213> Corynebacterium glutamicum

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55 Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala 45
 35 40

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu 60
 50 55

60 Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly 80
 65 70 75

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
85 90 95

5 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
100 105 110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
115 120 125

10 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
130 135 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
145 150 155 160

15 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
165 170 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
180 185 190

Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
195 200 205

25 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
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Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
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30 Gly Leu Glu His Tyr Leu Gly Leu
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35 <210> 4
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<213> Corynebacterium glutamicum

40 <220>
<223> dapA wild-type promoter

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45 <210> 5
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dapA promoter of C. glutamicum with the MC20 mutation

55 <220>
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<222> (45)

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- 5 <210> 6
- <211> 80
- <212> DNA
- <213> Synthetic sequence

- 10 <220>
- <223> Description of the synthetic sequence:
dapA promoter of C. glutamicum with the
MA16 mutation

- 15 <220>
- <221> mutation
- <222> (35)..(53)

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